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seq_name: gb_est2:BM078237

seq_documentation_block:
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DEFINITION MEST116-H10.T3 ISUM4-TN zea mays cDNA clone MEST116-H10 3', mRNA
sequence.
ACCESSION BM078237
VERSION BM078237.1 GI:16925169
KEYWORDS EST.
SOURCE zea mays.
ORGANISM zea mays.
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clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 685)
Qlu,F., Cul,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
phred software.
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
tc). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR PRIMERS
FORMARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAG)
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
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/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AAGTGAAGAATTCGGCGCGCAGGAATTTTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
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BASE COUNT 177 a 169 c 155 g 184 t
ORIGIN

alignment_scores:
Quality: 154.00 Length: 154
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x BM078237/rev ..

Align seg 1/1 to reverse of: BM078237 from: 1 to: 685

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634 CCAGGTGTGTTCAGGTGACGAGGATCTGTGCTTGAATGCCCTTCCAG 585
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seq_documentation_block:
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DEFINITION  660008A08.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
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ACCESSION  AM057042
VERSION    AM057042.1  GI:5932681
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 580)
AUTHORS   Walbot, V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
          University
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 660008 row: A column: 08.

FEATURES
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                   /organism="Zea mays"
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                   /db_xref="taxon:4577"
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                   /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
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                   Directionally sequenced with 5' end at the EcoRI site.
                   Created by Amie Franklin."

BASE COUNT      136 a      160 c      139 g      145 t
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481 TGGTGCCTTGATGCTTCGACAGCTTCACAGTTTCAACACCTCTTC 530
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seq_documentation_block:
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DEFINITION  MEST149-E08.T3 ISUM5-RN Zea mays cDNA clone MEST149-E08 3', mRNA
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ACCESSION  BM337351
VERSION    BM337351.1  GI:18167512
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 700)
REFERENCE  Wen, T.-J., Qiu, F., Guo, L., Ashlock, D. A and Schnable, P. S.
            Expressed Sequence Tags from B73 Maize: various stages and tissues
            including seedlings treated with a variety of hormones
            Unpublished (2001)
JOURNAL    Schnable Laboratory
            Iowa State University
            6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
            Tel: 515-294-0975
            Fax: 515-294-2299
            Email: schnable@iastate.edu
COMMENT    Individual basecall and confidence value were assigned using the
            Phred software.
            (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
            tr). Overall sequence quality assessment and vector trimming were
            conducted using the Lucy software (<http://www.tigr.org/softlab/>).
            Lucy parameters were set to ensure an overall trimmed quality of
            97.5% or better without any vector fragments in the chosen
            high-quality region of each sequence. Low-quality bases between the
            poly-T and the high-quality region were replaced with N's to serve
            as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
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                   Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
                   Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
                   (3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
                   ), tassels (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
                   cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated

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first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACP (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscissic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGGAAGATTCGGCCGAGCAATTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol- α -catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pRTT3AC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996).*

BASE COUNT 181 a 179 c 155 g 185 t
ORIGIN

alignment_scores:
Quality: 144.00 Length: 144
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x BM37351/rev ..

Align seg 1/1 to reverse of: BM37351 from: 1 to: 700

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seq_name: gb_est2:BM380735

seq_documentation_block:
LOCUS BM380735 670 bp mRNA linear EST 16-JAN-2002
DEFINITION M585524-C09.univ ISUM6 Zea mays cDNA clone M585524-C09 3', mRNA sequence.
ACCESSION BM380735
VERSION BM380735.1 GI:18179525
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 670)
Men,T.J., Qiu,F., Guo,L., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

Individual basculel and confidence value were assigned using the phred software(<http://www.phrap.org/>). Overall sequence quality assessment and vector trimming was conducted using the Lucy software (version 1.16s, <http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high quality region of each sequence. Low quality bases between the poly-T and the high quality region were replaced with N's to serve as spacers using a Perl program (est_process.pl), written by Dr. Hui-Hsien Chou.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG)
Seq primer: universal (GTA AAA CGA CGG CCA GT)
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..670
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="M585524-C09"
/clone_11b="ISUM6"
/tissue_type="mixed"
/lab_host="DH10B"
/note="Vector: pSLiP7 (4.43 kb); Site_1: EcoRI; Site_2: NotI; Tissue samples were collected and partially pooled prior to RNA extraction. First-strand cDNAs were prepared from 21 individual pools of oligo-dT selected mRNAs by priming with 21 different NotI oligo-dT tag primers (5'-AACTGGAAGATTCGGCCGAGCAATTTTCTTTT-3'). Distinguishable 'bar code' tags, (N)6, were used for each separate first-strand cDNA synthesis. Hence, these bar code tags can be used to identify the mRNA pool from which a particular cDNA clone was derived. The 'bar code' tags associated with specific tissue sources are:
ATAGCG--Germinated seeds and seedlings (1, 2, 8, 11 DAG);
ACTGCG--Mixed mature tissues (17, 21, 38, 69, 77 DAG);
CAGACG--Kernels (3, 5, 10, 15, 20, 25, 30, DAP);
TAACCC--Adventitious roots (65 DAG); CAGCG--Tassels (3-39 cm, 53 and 56 DAG); AGGTAC--Immature ears (0.2-3.0 cm, 53, 56, 59 DAG); TGAGCG--Husks (73 DAG); GACGAC--Silks;
AATGCG--unpollinated first ears; CTAGCG--ear shanks;
GAAGAC--etiolated seedlings; AGTGAG--callus;
GTGAGC--Cycloheximide-treated callus; GTGACC--Anaerobic treated seedlings; GATCCA--NAA (a-Naphthalene acetic acid)-treated seedlings; GATGCC--Kinetin-treated seedlings; AAGACG--ACPC (1-aminocyclopropane-1-carboxylic acid)-treated seedlings; GCCTCA--Brassinolide-treated seedlings; CTAGCG--ABA (Abscissic acid)-treated seedlings;

TACGGA--GA (Gibberellic acid)-treated seedlings;
 GCAGGA--JA (Jasmonic acid)-treated seedlings. Equal
 amounts of first-strand cDNA from each reaction were
 combined and used as template for DNA Pol-catalyzed 2nd
 strand synthesis. After the addition of EcoRI adaptors,
 ds-cDNAs were digested with NotI. Molecules between 0.5
 and 2.0 kb were directionally cloned into the EcoRI and
 NotI sites of the pSLIP7 expression vector. Plasmid DNA
 isolated from the library was digested with NotI to remove
 empty vector clones. Linear DNAs from 5.4 to 7 kb were gel
 purified and ligated at low concentration to promote
 recircularization. Ligation products were precipitated and
 transformed into DH10B host cells. The complexity of the
 resulting library was 1.2×10^6 .

BASE COUNT 172 a 170 c 148 g 180 t
 ORIGIN

alignment_scores:
 Quality: 137.00 Length: 137
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-805-550-2 x BM380735/rev ..

Align seg 1/1 to reverse of: BM380735 from: 1 to: 670

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265 ProGlyValValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgI 281
|||||
670 CCAGGCTGTGTCACAGATGCGATGCTGCTGATGCTGTCGACACA 621
|||||
281 nleuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnI 298
|||||
620 GCCTCCACAGATTCAAGCACTCCTTCAGTTCAGCCAGGCTTAATCCTCAA 571
|||||
298 leuGlnProMetLeuGlnGlnLeuGlyLysGlnAsnProGlnIleLeu 314
|||||
570 TCTTCGACGCCAATGCTTCAAGACCTGATTAACAAACCCACAAATTCCTG 521
|||||
315 ArgLeuIleGlnGlnAsnGlnAlaGlnPheLeuArgLeuAlaAsnGln 331
|||||
520 CGGTTATTCAGGAATATCAAGCTGAGTTCTCCGCTGGTGAATGATC 471
|||||
331 rProGlnGlyGlyProGlyLysAsnIleLeuGlyGlnLeuAlaAlaIav 348
|||||
470 TCCTGAGGGGTGCTCGAGAGGAACATACAGTCACATGCGACGTCGTG 421
|||||
348 aLProGlnThrLeuThrValThrProGlnGluArgGluAlaIleGlnArg 364
|||||
420 TGCCACAAACGCTGACAGTTACCCAGAGGAGGAGGAGCTATCCACAGCG 371
|||||
365 leuGlnGlyMetGlyPheAsnArgGluLeuValLeuGlnValPhePheAl 381
|||||
370 CTCGAGGGAATGGGTTCAACGCTGAGCTTGCTTAAGATTTTCTTGTGC 321
|||||
381 acysAsnIlyAspGluLeuThrAlaAsnTYrLeuLeuAspHisGlyH 398
|||||
320 ATGCAACAAGAGGAGAGCTTACAGCCACATCTCCTGATCATATGCC 271
|||||
398 lsgluPheasp 401
|||||
270 ATGAGTTTTCAC 260

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seq_name: gb_est1:A1947481

seq_documentation_block:
 LOCUS A1947481 497 bp mRNA linear EST 19-AUG-1999
 DEFINITION 614047B04.x1 614 - root cDNA library from Walbot Lab. Zea mays cDNA,
 mRNA sequence.
 ACCESSION A1947481
 VERSION A1947481.1 GI:5739686
 KEYWORDS EST.

SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 497)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 614047 row: B column: 04.
 Location/Qualifiers

FEATURES
 source
 1..497
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="614 - root cDNA library from Walbot Lab"
 /tissue_type="root"
 /dev_stage="3-4 days old"
 /lab_host="XILOR"
 /note="Organ: root; Vector: pBluescriptII SK+; Site_1:
 EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
 Lab (LW)"

BASE COUNT 117 a 137 c 121 g 121 t 1 others
 ORIGIN

alignment_scores:
 Quality: 133.00 Length: 133
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-805-550-2 x A1947481/rev ..

Align seg 1/1 to reverse of: A1947481 from: 1 to: 497

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269 ProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProGlnP 285
|||||
484 CCAGTCTGATGATTCGTCGCTTGAATGCTTCCGCCACGCTTCNCAGTT 435
|||||
285 egAlaLeuLeuGlnLeuValGlnAlaAsnProGlnIleLeuGlnProm 302
|||||
434 TCAAGCACTCCTTCAGTTCAGTTCAGGCTTAATCCTCAATGCTTGCAGCCAA 385
|||||
302 etLeuGlnGlnLeuGlyLysGlnAsnProGlnIleLeuArgLeuIleGln 318
|||||
384 TGCCTTCAAGAGCTGATTAACAAACCCCAAAATTCGCGGTTGATTCAG 335
|||||
319 GlnAsnGlnAlaGlnPheLeuArgLeuValAsnGlnSerProGlnGly 335
|||||
334 GAAATATCAAGCTGAGTTTCTCCGCTTGATGATTAATCTCTGAGGTTG 285
|||||
335 yProGlyLysAsnIleLeuGlnGlnLeuAlaAlaValProGlnThrL 352
|||||
284 TCCTGAGAGGAACATACAGTCAATGCGCAGCTGCTGCGCCAAACGC 235
|||||
352 eutThrValThrProGlnGluArgGluAlaIleGlnArgLeuGlyMet 368
|||||
234 TGAAGTTACCCAGAGGAACGAGGAGCTATCCAGCGGCTCGAGGAGATG 185
|||||
369 GlyPheAsnArgGluLeuValLeuGluValPhePheAlaCysAsnLys 385
|||||
184 GGGTTCAACCGTGAAGCTTGTGCTGAAGTTTCTTTCGATGCAACAAGA 135
|||||
385 pGluGlnLeuThrAlaAsnTYrLeuLeuAspHisGlyHisGluPheasp 401

```


kinetin-treated seedlings, ACPC (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, brassinolide-treated seedlings, ABA (abscisic acid)-treated seedlings, GA (gibberellic acid)-treated seedlings, JA (jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGGAGAAATTCGCGCCGACGAGAAATTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pTZ19PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcello Bento Soares (genome Research 6: 791-806, 1996).

BASE COUNT 167 a 169 c 147 g 180 t
ORIGIN

alignment_scores:
Quality: 133.00 Length: 133
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x BM26651/rev ..

Align seg 1/1 to reverse of: BM26651 from: 1 to: 663

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269 ProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgInleuProGlnPh 285
|||||
662 CAGGTGCAAGACTGTGCTGCTGATGACCTTGCGACAGCTTCACAGTT 613
|||||
285 eGlnAlaLeuLeuGlnleuValGlnAlaAsnProGlnInleuGlnProm 302
|||||
612 TCAGCACCTCTTCAGTTAGTCCAGGCTAATCCCAATCTTGCAGCCAA 563
|||||
302 etLeuGlnleuLeuGlyLysGlnAsnProGlnInleuArgleuIleGln 318
|||||
562 TGCTTCAAGAGCTAGTAAACCAACCAATTCGCGTTGATTCAG 513
|||||
319 GlnAsnGlnAlaGlnPheLeuArgleuValAsnGlnSerProGlnIleG 335
|||||
512 GAAATCAAGCTGAGTTTCGCTGCTGATGATCAATCTCTGAGGTTG 463
|||||
335 yProGlyGlyAsnIleLeuGlyGlnleuAlaAlaValProGlnThrL 352
|||||
462 TCTTGGAGGGAACATAGTCAACTGCGAGCTGCTGCGCAACACGC 413
|||||
352 eutThrValThrProGlnGlnArgleuAlaIleGlnArgleuGlnIle 368
|||||
412 TGACAGTACCCAGAGGAACGGAGGCTATCCAGCGCTGAGGGAATG 363
|||||
369 GlyPheAsnArgleuLeuValleuGlnValPhePheAlaCysAsnLys 385
|||||
362 GGGTTCAACCGTGAAGCTTGTGCTGAAGTTTCTTTCGATCAACAAGA 313
|||||
385 pGlnGlnleuThrAlaAsnTyrlleuLeuAspHisGlyHisGlnPhe 401
|||||
312 CGAAGACCTTACAGCCAACTACCTCGATCAGATCAGCCATGATTGAC 264
|||||
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seq_name: gb_est1:AI759136

seq_documentation_block:

LOCUS AI759136 530 bp mRNA linear EST 02-FEB-2000
DEFINITION 605085tel1.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
CDNA, mRNA sequence.
ACCESSION AI759136
VERSION AI759136.1 GI:5152838
KEYWORDS EST.

SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 530)
AUTHORS Walbot,V.
TITLE Malze Ests from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 605085 row: E column: 11.
Location/Qualifiers
1. 530
/organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site: 1; EcoRI;
Site2: XhoI; Kernel endosperm cDNA library from Schmidt
lab"

FEATURES
source

BASE COUNT 137 a 135 c 121 g 137 t
ORIGIN

alignment_scores:
Quality: 117.00 Length: 117
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x AI759136/rev ..

Align seg 1/1 to reverse of: AI759136 from: 1 to: 530

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285 PheGlnAlaLeuLeuGlnleuValGlnAlaAsnProGlnInleuGlnPr 301
|||||
529 TTTCAAGACACTCTTCACTTACTAGCTCAAGCTAATCTCAATCTTCAG 480
|||||
301 oMetLeuGlnleuLeuGlyLysGlnAsnProGlnInleuArgleuIleG 318
|||||
479 AATGCTTCAAGAGCTAGTAAACCAACCCCAATTCGCGGTGATTC 430
|||||
318 lnglAsnGlnAlaGlnPheLeuArgleuValAsnGlnSerProGlnIle 334
|||||
429 AGGAAATCAAGCTGAGTTTCGCTGCTGATGAAAGAAATCTCTGAGGCT 380
|||||
335 GlyProGlyGlyAsnIleLeuGlyGlnleuAlaAlaValProGlnThr 351
|||||
379 GCTCTGAGAGGAACATAGTCAACTGCGAGCTGCTGCGCAACAC 330
|||||
351 rLeuThrValThrProGlnGlnArgleuAlaIleGlnArgleuGlnIle 368
|||||
329 GCTGACACTTACCCAGAGGAACGGAGGCTATCCAGCGGCTCGAGGGA 280
|||||
368 etGlyPheAsnArgleuLeuValleuGlnValPhePheAlaCysAsnLys 384
|||||
279 TGGGTTCAACCGTGAAGCTTGTGCTGAAGTTTCTTTCGATCAACAAG 230
|||||
385 AspGlnGlnleuThrAlaAsnTyrlleuLeuAspHisGlyHisGlnPhe 401
|||||
229 GACGAGAGCTTACAGCACTACTCTCTGATCATTGCGCATGAGTTTGA 180
|||||
```

401 p 401

Brassinolide-treated seedlings, ABA (Abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGGAGATTCGGCCGACGAGAAATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

BASE COUNT 147 a 151 c 124 g 166 t

ORIGIN

alignment_scores:

Quality: 106.00 Length: 106
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x BM075107/rev ..

Align seg 1/1 to reverse of: BM075107 from: 1 to: 588

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296 ProGlnIleuGlnProMetIleuGlnIleuGlyLysGlnAsnProGln 312
|||||
587 CCTCAAAATCTTCAGGCAATGCTTCAAGAGCTAGTAAACAAACCCACA 538
312 nIleuArgLeuIleGlnIleuAsnGlnIleuValPheLeuArgLeuVal 329
|||||
537 AATTCTGCGGTGATTCAAGAAATCAAGCTGAGTTCTCCGCTTGATGA 488
329 snGluSerProGluGlyGlyProGlyGlyAsnIleuGlnIleuAla 345
|||||
487 ATGAATCTCTGAGGGGTGCTCTGAGGGAACACTAGGTCAACGGCA 438
346 AlaAlaValProGlnThrLeuThrValThrProGluGlnArgIleuAla 362
|||||
437 GCTGCTGTCTCCACAAACGCTGACAGTACCACAGAGAAAGGAGCTAT 388
362 eGlnArgLeuGlnGlyMetGlyPheAsnArgGluLeuValIleuGlnVal 379
|||||
387 CCAGCGGCTCGAGGAGATGGGTTCACCGGTGAGCTTGCTGAAGATT 338
379 hspPheIaCysAsnIysAspGluGluLeuThrAlaAsnTyrIleuLeuAsp 395
|||||
337 TCTTTGCATGCAACAGAGCAAGAGACTTACAGCCAACTACCTCCGTGAT 288
396 HisGlyHisGluPheAsp 401
|||||
287 CATGGCCATGAGTTTGAC 270
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seq_name: gb_est1:AI783295

seq_documentation_block:

LOCUS AI783295 382 bp mRNA linear EST 01-JUL-1999
DEFINITION 614010B04.x2 614 - root cDNA library from Walbot Lab Zea mays cDNA,
mRNA sequence.

ACCESSION AI783295
VERSION AI783295.1 GI:5325104

KEYWORDS EST.
SOURCE Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 382)

AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614010 row: B column: 04.
Location/Qualifiers

FEATURES

source

1..382

/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/rlnsue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site: 1:
EcoRI; Site: 2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
Lab (LM) 92 a 97 c 101 g 92 t

BASE COUNT 92 a 97 c 101 g 92 t

ORIGIN

alignment_scores:

Quality: 105.00 Length: 105
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x AI783295 ..

Align seg 1/1 to: AI783295 from: 1 to: 382

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269 ProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProGlnP 285
|||||
68 CCAGGCTCTGATCTGGTGGCCTTGATGCTTGCGACAGCTTCACAGTT 117
285 eGlnAlaLeuGlnIleuValGlnAlaAsnProGlnIleuGlnProM 302
|||||
118 TCAAGCACTCCTTCAGTTAGTCCAGGCTAATCTCAATCTTCGAGCA 167
302 etLeuGlnIleuGlyGlyGlnAsnProGlnIleuArgLeuIleGln 318
|||||
168 TGGTTCAGAGCTAGTAAACAAACCCAAATCTGCGGTGATTGATCAG 217
319 GluAsnGlnIleuGlnPheLeuArgLeuValAsnGluSerProGluGly 335
|||||
218 GAAATCAACTGAGTTCTCCGCTTGCTGAATGAATCTCTGAGGGTGG 267
335 yProGlyGlyAsnIleuGlnIleuAlaAlaValProGlnThrL 352
|||||
268 TCCTGAGAGGAAACATAGTCAACTGCGAGCTGCTGCCACAAACGC 317
352 eurThrValThrProGluGlnArgGlnAlaIleGlnArgLeuGlnGlyMet 368
|||||
318 TGACAGTTACCCCGAGAGAAAGGAGGCTATCCAGCGGCTCGAGGAGATG 367
369 GlyPheAsnArgGlu 373
|||||
368 GGGTTCACCGCTGAG 382
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seq_name: gb_est2:BI991866

seq_documentation_block:

LOCUS BI991866 609 bp mRNA linear EST 24-OCT-2001
DEFINITION 1020052G08.x1 1020 - unigene II from Maize Genome Project Zea mays
cDNA, mRNA sequence.
ACCESSION BI991866

VERSION B1991866.1 GI:16377325
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 609)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished (1999)
 CONTACT: Walbot V
 DEPARTMENT OF Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1020052 row: G column: 08.
 Location/Qualifiers
 1..609
 /organism="Zea mays"
 /db_xref="taxon:4577"
 /clone_lib="1020 - Unigene II from Maize Genome Project"
 /note="This library represents the unique genes found in
 the second round of EST sequencing at Stanford University
 for the maize genome project. Sequences are present from
 libraries 947 and 949. Contigs were assembled using
 zmbAssembler and 2 representatives from each contig were
 selected for the unigene set. All singlets were also
 selected."
 BASE COUNT 168 a 158 c 129 g 154 t
 ORIGIN
 alignment_scores:
 Quality: 104.00 Length: 104
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-805-550-2 x B1991866/rev ..
 Align seg 1/1 to reverse of: B1991866 from: 1 to: 609
 298 lileuglnpmetleuglnleuglnleuglnleuglnleuglnle 314
 |||
 609 AMCTTGACGCAATGCTCAAGAGCTAGTAAGCAAAACCCCAATCT 560
 314 uArgleuileuglnleuglnleuglnleuglnleuglnleugln 331
 |||
 559 GCGGTTGATTAGGAAATCAAGCTGAGTTCTCGCTTGGAATGAA 510
 |||
 331 ePProgluIGlyProgluGlyAsnileuglnleuglnleuglnle 347
 |||
 509 CTCCTGAGGAGTGTCTGAGGGAACATAGGTCACCTGCACTGCT 460
 |||
 348 ValProglInthrleuthrValThrProgluGluArgGluAlaIle 364
 |||
 459 GTGCACAAACGCTGACAGCTTACCCACAGAGAGCGAGGCTATCC 410
 |||
 364 gLeugluGlyMetGlyPheAsnArgGluLeuValleuglnValPhe 381
 |||
 409 GCTGAGAGGAATGGGTTCAACCGTGAAGCTTGCTAGAAATTTCT 360
 |||
 381 lAcysAsnleuAspGluGluLeuThrAlaAsnTyrleuLeuAspHis 397
 |||
 359 CATCAACACAAAGAGAGAGCTTACAGCACTACCTCTGATCATGAC 310
 |||
 398 HisGluPheAsp 401
 |||
 309 CATGAGTTGAC 298

seq_name: gb_est1:AM155658
 seq_documentation_block:
 LOCUS AM155658 589 bp mRNA linear EST 04-NOV-1999
 DEFINITION 614097D11.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
 mRNA sequence.
 ACCESSION AM155658
 VERSION AM155658.1 GI:6227129
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished (1999)
 CONTACT: Walbot V
 DEPARTMENT OF Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 614097 row: D column: 11.
 Location/Qualifiers
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 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="614 - root cDNA library from Walbot Lab"
 /issue_type="root"
 /dev_stage="3-4 days old"
 /lab_host="XOIR"
 /note="Organ: root; Vector: pBluescriptII SK+; Site: 1:
 EcoRI; Site: 2: XhoI; 3-4 days old root tissue from Walbot
 Lab (LM)"
 BASE COUNT 139 a 169 c 139 g 140 t 2 others
 ORIGIN
 alignment_scores:
 Quality: 100.00 Length: 100
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-805-550-2 x AM155658 ..
 Align seg 1/1 to: AM155658 from: 1 to: 589
 160 leuglnGlnThrIleGlnGlnIleleuAspMetGlyGlyGlyThrTrp 176
 |||
 168 CTAGACAGACATATCCAAATCTTGACATGGGTGGTATGAGGA 217
 |||
 176 uArgAspThrValValArgAlaLeuArgAlaAlaIleThrAsnAsnPro 193
 |||
 218 ACGTATATACAGTTGTTCTGCTGCTCTGCTGCTGCTGCTGCTG 267
 |||
 193 rGAlaIleAspTyrleuTyrSerGlyIleProGluAsnValGluAla 209
 |||
 268 GAGCATATAGACTACTGATTTCTGGAATTCGGAATGTGAGGCTCAG 317
 |||
 210 ProValAlaArgAlaProAlaAlaGlyGlnGlnThrAsnGlnAlaAl 226
 |||
 318 CCGTGTGCCCGAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
 |||
 226 aserProAlaGlnProAlaValAlaLeuProValGlnProSerProAl 243
 |||
 368 ATCACCCGCTCAGCCAGCATGTTGCAATGCTGAGGAGCCATCCTGCT 417

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243 ealAlaGlyProAsnAlaAsnProLeuAsnLeuPheProGlnGlyValPro 259
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418 CTCGAGGGCGCTAATGCAAAATCTTTGAACTTTTCTCGAGGTTGCA 467

seq_name: gb_est1:AI834654

seq_documentation_block:
LOCUS      AI834654          495 bp      mRNA      linear      EST 02-FEB-2000
DEFINITION 606071D12.x1 606 - Ear tissue cDNA library from Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION  AI834654
VERSION     AI834654.1  GI:5468863
KEYWORDS   EST.
SOURCE      Zea mays.
            Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 495)
AUTHORS     Walbot,V.
TITLE       Maize ESTs from various cDNA libraries sequenced at Stanford
            University
JOURNAL     Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 606071 row: D column: 12.
FEATURES
source
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            /cultivar="Ohio43"
            /db_xref="taxon:4577"
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            lab"
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            /dev_stage="ear length from 0.5 cm - 2.0 cm"
            /lab_host="XLOLR (Stratagene)"
            /note="Organ: Immature ear; Vector: pBK-CMV; Site_1: EORI
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BASE COUNT  125 a      129 c      103 g      138 t
ORIGIN
alignment_scores:
Quality:      89.00      Length:      89
Ratio:        1.000      Gaps:        0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x AI834654/rev ..

Align seg 1/1 to reverse of: AI834654 from: 1 to: 495

313 lIleuAArgLeuIleGlnGluAsnGlnAlaGluPheLeuAArgLeuValAs 329
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494 ATTCTGCGGTGATTCAGAAAAATCAAGCTGAGTTCTCGCTTGAGAA 445

329 ngIuSerProGluGlyGlyProGlyGlyAsnIleLeuGlnIleuAlaA 346
|||||
444 TGAATCTCTGAGAGGTGCTCTGAGGGAACATACCTAGCTCACTGGCAG 395

346 lAlaIValProGlnThrLeuThrValThrProGluGluAArgGluAlaIle 362
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394 CTGCTGTGCCACAACGCTGACAGTTACCCAGAGAAACGAGAGGCTATC 345

363 GlnAArgLeuGluMetGlyPheAsnAArgGluLeuValLeuGluValPh 379
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344 CAGCGCTCCAGAGGATGGGTTCAACCGTGAGCTTGCTAGAGTTT 295
379 ePheAlaCysAsnLysAspGluGluLeuThrAlaAsnTyrLeuLeuAspH 396
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294 CTTTGCAATGCACAAGAGCGAAGAGCTTACAGCCAACTACTCTCTGATC 245
396 lSgIyHlSgIuPheAsp 401
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244 ATGGCCATGAGTTTGAC 228

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